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APPLICATION NOTE

Automated digestion of Albumin from Bovine serum, Chicken egg and Human serum. Using StyrosZyme® TPCK-Trypsin, Immobilized Enzyme on Polymeric Hard Gel Simulated-Monolith™ Enzyme Reactor with the Acquity UPLC *I* class Plus and Final Silica mapping.

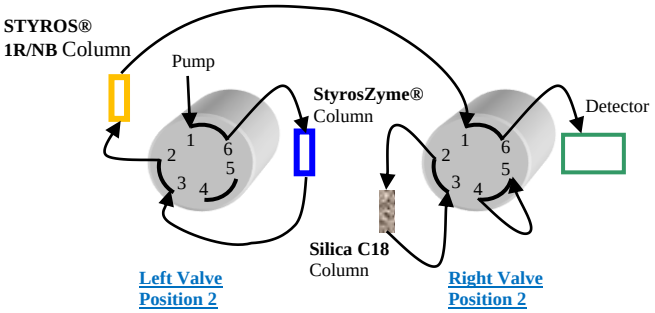
Extensive digestion of human serum albumin with trypsin at pH 8.8 yields essentially one main fragment which is resistant to further tryptic degradation.
Repeated digestion does not degrade the isolated fragment further. The fragment mainly retains the secondary and tertiary structure of intact human serum albumin.
These results are from batch digestion with trypsin.

We have compared these results to the automated online digestion during which the autodigestion of trypsin is avoided therefore retaining its full activity during the process.

The buffers used are.
Buffer A: 0.1 % TFA in DI H2O: ACN 98:2 (for peptide mapping)
Buffer B: 0.1 % TFA in ACN: H2O, 70:30 (for peptide mapping)
Buffer C: 0.1 M Tris, 0.15 M NaCl pH= 8.55 (for digestion).

The 3 columns used are all narrow bore, therefore minimizing high solvent consumption as well as generation of waste
An Enzyme column of 2.1x100 mm stainless Steel (StyrosZyme® TPCK-Trypsin).
Two narrow bore reversed phase columns. One polymeric (STYROS® 1R) with high capacity and high pH tolerance and one Silica C18 column (Acquity UPLC® BEH C18 1.7 µm 2.1x50 cm column) with high performance.

The following shows the starting position of the valves used:



Setup 1

In this first position, the StyrosZyme® enzyme column and the polymeric STYROS® 1R/NB column only, are online and the Silica C18 column is not exposed to any high pH aqueous buffer that is used for the digestion.
It is therefore possible to safely scout the right digestion buffer as well as the optimum conditions for the full digestion prior to the use of the silica column.
Both polymeric columns, StyrosZyme® TPCK-Trypsin and STYROS® R reversed phase polymeric can tolerate high pH.

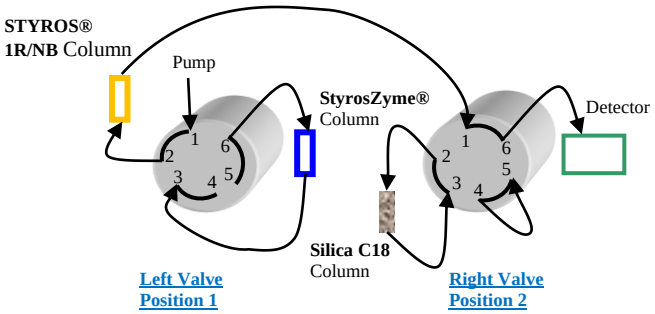
1-Equilibrate the enzyme column with all columns except the silica column, in line, as shown in Setup 1.

Time	% of buffer C	Flow rate (ml/min)
0		0
0.01	100	0.2
6	100	0.2

2-With both columns in line as in Setup 1, 0.2 µl of a solution of 10 mg/ml protein in buffer A is injected, and the resulting digests are dumped on the reversed phase polymeric column using the following method:

Time	% of buffer C	Flow rate (ml/min)
0		0
0.01	100	0.1
10	100	0.1

In the second set up, the left valve is switched to position 1 with only the STYROS® 1R reversed phase column online to equilibrate it with the starting solvent gradient.



Setup 2

3-The reversed phase Polymeric column only is now in line as in Setup 2 to wash the leftover salt and prepare it for the reversed phase mapping.

It is also ready for hyphenation with a mass spectrometer.

Time	% of buffer B	% of buffer A	Flow rate (ml/min)
0			0
0.01	0	100	0.3
10	0	100	0.3

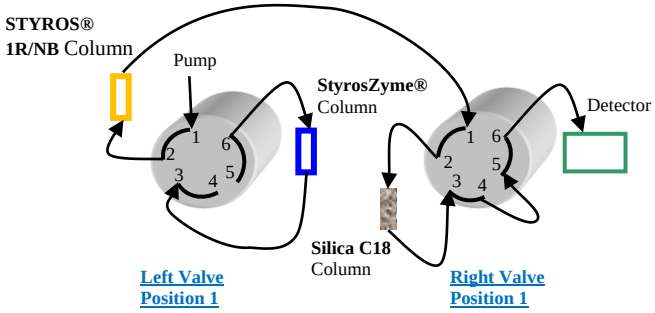
4-The digested peptides are now trapped on the polymeric reversed phase column and can be mapped following a gradient.
The setup is now as Setup 2.

Time	% of buffer B	% of buffer A	Flow rate (ml/min)
0			0
0.01	0	100	0.2
20	70	30	0.2

Once the conditions of the digestion are satisfactory, one can use the second switching valve to bring the Silica C18 column online as shown in Setup 3.
The same gradient as in step 4 can be used for the mapping to run the separation on the C18 Silica column in addition:

4'-The digested peptides trapped on the polymeric reversed phase column can now be mapped on the C18 Silica column in addition.
The setup is now as Setup 3.

Time	% of buffer B	% of buffer A	Flow rate (ml/min)
0			0
0.01	0	100	0.2
20	70	30	0.2



Setup 3

4''-In this step, using the same setup 3, the columns are washed with high organic to make sure they are devoid of any leftover proteinaceous species.
The setup remains Setup 3.

Time	% of buffer B	% of buffer A	Flow rate (ml/min)
0			0
0.01	60	40	0.3
2	100	0	0.3
4	0	100	0.3
8	0	100	0.3

To re-equilibrate both reversed phase columns that are now in line, the following step 5 is used.

5- Both reversed phase columns are preequilibrated to the initial low organic prior to getting in contact with the digestion buffer.
The setup is now Setup 3.

Time	% of buffer B	% of buffer A	Flow rate ml/min
0			0
0.01	0	100	0.3
10	0	100	0.3

6-In the final step the line and the reversed phase column are flushed clean from any leftover organic going to the enzyme column, still avoiding the Silica column. The setup therefore remains as setup 2.

Time	% of digestion buffer C	Flow rate (ml/min)
0		0
0.01	100	0.3
6	100	0.3

The system is now ready for the next cycle to check the reproducibility of the digestion.

We have used 0.2 µl of a solution of 10 mg/ml of protein in buffer A as sample to digest.
The temperature is set at 37°C for all sequences.

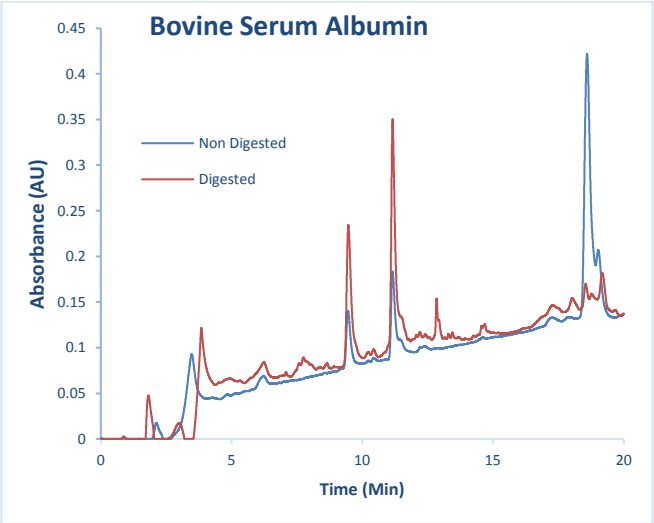
We have compared 3 albumins: from bovine serum, chicken egg albumin and human serum albumin and compared them to one another.
The digestions are done under similar conditions
The enzyme column of 2.1 x 100 mm has a volume to 0.346 ml. A total of 1 ml is run through it during the digestion at a volumetric flow of 0.1 ml/min.

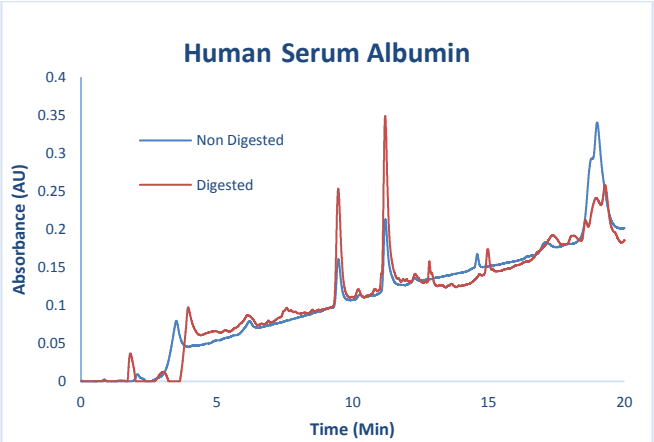
Each digest is compared with the corresponding starting intact protein.
All three albumins display a similar pattern of major fragments included in them. Those fragments become more concentrated during the digestion.
Other fragments do appear at the expense of the last peak in the sample albumin as well.
The digestion with immobilized StyrosZyme® TPCK-Trypsin does alter all three albumins from different sources.

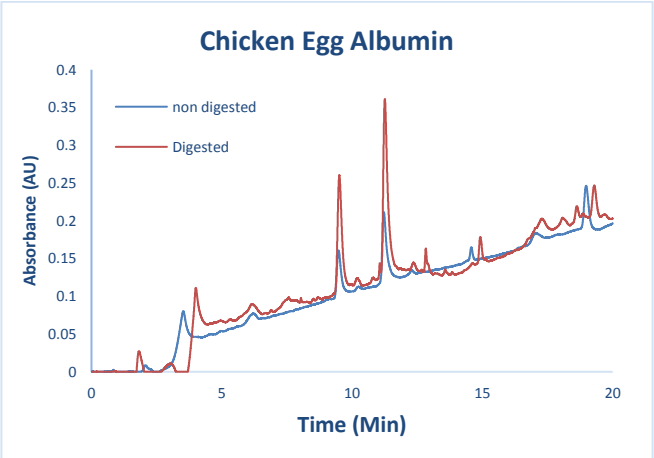
Comparing the starting proteins with each other, a similar pattern emerges except for the last peak of the chromatogram run with the combination of STYROS® 1R polymeric and Acquity UPLC® BEH C18 run in series.

The same similarity is noticed in the digested proteins. The same peaks that were present at the start are enhanced following the digestion.

The performance of the STYROS® 1R polymeric is crucial in the final separation of the digested peptides,







The digestion is advanced in all three cases.